SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT:
      (A) NAME: MOGEN INTERNATIONAL NV
      (B) STREET: Einsteinweg 97
      (C) CITY: Leiden
      (E) COUNTRY: The Netherlands
      (F) POSTAL CODE (ZIP): 2233 CB
      (G) TELEPHONE: (31) 71-5258282
      (H) TELEFAX: (31) 71-5221471

   (ii) TITLE OF INVENTION: Enhanced accumulation of trehalose in plants

   (iii) NUMBER OF SEQUENCES: 27

   (iv) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Floppy disk
      (B) COMPUTER: IBM PC compatible
      (C) OPERATING SYSTEM: PC-DOS/MS-DOS
      (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

   (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2621 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA to mRNA

   (iii) HYPOTHETICAL: NO

   (ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 25..2485
      (D) OTHER INFORMATION: /function= "trehalose phosph.
          synthase and trehalose phosph. phosphatase"
          /product= "bipartite enzyme"

   (ix) FEATURE:
      (A) NAME/KEY: unsure
      (B) LOCATION: 1609..1611

29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CTGATCCTGC GGTTTCATCA CAAT ATG ATA CTC TTA CAT CTG ATG CCC CTT          51
                            Met Ile Leu Leu His Leu Met Pro Leu
  5                          1                   5

     CAG ATG CTC CCA AAT AGG TTG ATT GTC GTA TCG AAT CAG TTA CCC ATA       99
     Gln Met Leu Pro Asn Arg Leu Ile Val Val Ser Asn Gln Leu Pro Ile
     10              15                  20                  25
 10

     ATC GCT AGG CTA AGA CTA ACG ACA ATG GAG GGT CCT TTT GGG ATT TCA      147
     Ile Ala Arg Leu Arg Leu Thr Thr Met Glu Gly Pro Phe Gly Ile Ser
                     30                  35                  40

 15  CTT GGG ACG AGA GTT CGA TTT ACA TGC ACA TCA AAG ATG CAT TAC CCG      195
     Leu Gly Thr Arg Val Arg Phe Thr Cys Thr Ser Lys Met His Tyr Pro
                     45                  50                  55

     CAG CCG TTG AGG TTT TCT ATT CTT GGC GAT CCA CTA AGG GCT GAC GTT      243
 20  Gln Pro Leu Arg Phe Ser Ile Leu Gly Asp Pro Leu Arg Ala Asp Val
                 60                  65                  70

     GGC CCT ACC GAA CAA GAT GAC GTG TCA AAG ACA TTG CTC GAT AGG TTT      291
     Gly Pro Thr Glu Gln Asp Asp Val Ser Lys Thr Leu Leu Asp Arg Phe
 25      75                  80                  85

     AAT TGC GTT GCG GTT TTT GTC CCT ACT TCA AAA TGG GAC CAA TAT TAT      339
     Asn Cys Val Ala Val Phe Val Pro Thr Ser Lys Trp Asp Gln Tyr Tyr
     90                  95                  100                 105
 30

     CAC TGC TTT TGT AAG CAG TAT TTG TGG CCG ATA TTT CAT TAC AAG GTT      387
     His Cys Phe Cys Lys Gln Tyr Leu Trp Pro Ile Phe His Tyr Lys Val
                     110                 115                 120

 35  CCC GCT TCT GAC GTC AAG AGT GTC CCG AAT AGT CGG GAT TCA TGG AAC      435
     Pro Ala Ser Asp Val Lys Ser Val Pro Asn Ser Arg Asp Ser Trp Asn
                     125                 130                 135

     GCT TAT GTT CAC GTG AAC AAA GAG TTT TCC CAG AAG GTG ATG GAG GCA      483
 40  Ala Tyr Val His Val Asn Lys Glu Phe Ser Gln Lys Val Met Glu Ala
             140                 145                 150

     GTA ACC AAT CGT AGC AAT TAT GTA TGG ATA CAT GAC TAC CAT TTA ATG      531
     Val Thr Asn Arg Ser Asn Tyr Val Trp Ile His Asp Tyr His Leu Met
 45      155                 160                 165

     ACG CTA CCG ACT TTC TTG AGG CGG GAT TTT TGT CGT TTT AAA ATC GGT      579
     Thr Leu Pro Thr Phe Leu Arg Arg Asp Phe Cys Arg Phe Lys Ile Gly
     170                 175                 180                 185
 50

     TTT TTT CTG CAT AGC CCG TTT CCT TCC TCG GAG GTT TAC AAG ACC CTA      627
     Phe Phe Leu His Ser Pro Phe Pro Ser Ser Glu Val Tyr Lys Thr Leu
                     190                 195                 200
```

```
     CCA ATG AGA AAC GAG CTC TTG AAG GGT CTG TTA AAT GCT GAT CTT ATC    675
     Pro Met Arg Asn Glu Leu Leu Lys Gly Leu Leu Asn Ala Asp Leu Ile
             205             210             215

  5  GGG TTC CAT ACA TAC GAT TAT GCC CGT CAT TTT CTA ACG TGT TGT AGT    723
     Gly Phe His Thr Tyr Asp Tyr Ala Arg His Phe Leu Thr Cys Cys Ser
             220             225             230

     CGA ATG TTT GGT TTG GAT CAT CAG TTG AAA AGG GGG TAC ATT TTC TTG    771
 10  Arg Met Phe Gly Leu Asp His Gln Leu Lys Arg Gly Tyr Ile Phe Leu
             235             240             245

     GAA TAT AAT GGA AGG AGC ATT GAG ATC AAG ATA AAG GCG AGC GGG ATT    819
     Glu Tyr Asn Gly Arg Ser Ile Glu Ile Lys Ile Lys Ala Ser Gly Ile
 15  250             255             260             265

     CAT GTT GGT CGA ATG GAG TCG TAC TTG AGT CAG CCC GAT ACA AGA TTA    867
     His Val Gly Arg Met Glu Ser Tyr Leu Ser Gln Pro Asp Thr Arg Leu
                     270             275             280
 20
     CAA GTT CAA GAA GTC CAA AAA CGT TCG AAG GAA ATC GTG CTA CTG GGA    915
     Gln Val Gln Glu Val Gln Lys Arg Ser Lys Glu Ile Val Leu Leu Gly
                 285             290             295

 25  GTT GAT GAT TTG GAT ATA TTC AAA GGT GTG AAC TTC AAG GTT TTA GCG    963
     Val Asp Asp Leu Asp Ile Phe Lys Gly Val Asn Phe Lys Val Leu Ala
             300             305             310

     TTG GAG AAG TTA CTT AAA TCA CAC CCG AGT TGG CAA GGG CGT GTG GAA   1011
 30  Leu Glu Lys Leu Leu Lys Ser His Pro Ser Trp Gln Gly Arg Val Glu
             315             320             325

     AAG GTG CAA ATC TTG AAT CCT CTG CGC CGT TGC CAA GAC GTC GAT GAG   1059
     Lys Val Gln Ile Leu Asn Pro Leu Arg Arg Cys Gln Asp Val Asp Glu
 35  330             335             340             345

     ATC AAT GCC GAG ATA AGA ACA GTC TGT GAA AGA ATC AAT AAC GAA CTG   1107
     Ile Asn Ala Glu Ile Arg Thr Val Cys Glu Arg Ile Asn Asn Glu Leu
                 350             355             360
 40
     GGA AGC CCG GGA TAC CAG CCC GTT GTG TTA ATT GAT GGG CCC GTT TCG   1155
     Gly Ser Pro Gly Tyr Gln Pro Val Val Leu Ile Asp Gly Pro Val Ser
             365             370             375

 45  TTA AGT GAA AAA GCT GCT TAT TAT GCT ATC GCC GAT ATG GCA ATT GTT   1203
     Leu Ser Glu Lys Ala Ala Tyr Tyr Ala Ile Ala Asp Met Ala Ile Val
             380             385             390

     ACA CCG TTA CGT GAC GGA CTG AAT CTT ATC CCG TAC GAG TAC GTC GTT   1251
 50  Thr Pro Leu Arg Asp Gly Leu Asn Leu Ile Pro Tyr Glu Tyr Val Val
             395             400             405
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```
          TCC CGA CAA AGT GTT AAT GAC CCA AAT CCC AAT ACT CCA AAA AAG AGC     1299
          Ser Arg Gln Ser Val Asn Asp Pro Asn Pro Asn Thr Pro Lys Lys Ser
          410             415             420             425

  5       ATG CTA GTG GTC TCC GAG TTC ATC GGT GTT TCA CTA TCT TTA ACC GGG     1347
          Met Leu Val Val Ser Glu Phe Ile Gly Val Ser Leu Ser Leu Thr Gly
                          430             435             440

          GCC ATA CGG GTC AAC CCA TGG GAT GAG TTG GAG ACA GCA GAA GCA TTA     1395
  10      Ala Ile Arg Val Asn Pro Trp Asp Glu Leu Glu Thr Ala Glu Ala Leu
                          445             450             455

          TAC GAC GCA CTC ATG GCT CCT GAT GAC CAT AAA GAA ACC GCC CAC ATG     1443
          Tyr Asp Ala Leu Met Ala Pro Asp Asp His Lys Glu Thr Ala His Met
  15          460             465             470

          AAA CAG TAT CAA TAC ATT ATC TCC CAT GAT GTA GCT AAC TGG GCT AGC     1491
          Lys Gln Tyr Gln Tyr Ile Ile Ser His Asp Val Ala Asn Trp Ala Ser
              475             480             485
  20
          TTC TTT CAA GAT TTA GAG CAA GCG TGC ATC GAT CAT TCT CGT AAA CGA     1539
          Phe Phe Gln Asp Leu Glu Gln Ala Cys Ile Asp His Ser Arg Lys Arg
          490             495             500             505

  25      TGC ATG AAT TTA GGA TTT GGG TTA GAT ACT AGA GTC GTC TTT TTG ATG     1587
          Cys Met Asn Leu Gly Phe Gly Leu Asp Thr Arg Val Val Phe Leu Met
                          510             515             520

          AGA AGT TTA GCA AGT TGG ATA AAG ATG TCT TGG AAG AAT GCT TAT TCC     1635
  30      Arg Ser Leu Ala Ser Trp Ile Lys Met Ser Trp Lys Asn Ala Tyr Ser
                          525             530             535

          ATG GCT CAA AAT CGG GCC ATA CTT TTG GAC TAT GAC GGC ACT GTT ACT     1683
          Met Ala Gln Asn Arg Ala Ile Leu Leu Asp Tyr Asp Gly Thr Val Thr
  35          540             545             550

          CCA TCT ATC AGT AAA TCT CCA ACT GAA GCT GTT ATC TCC ATG ATC AAC     1731
          Pro Ser Ile Ser Lys Ser Pro Thr Glu Ala Val Ile Ser Met Ile Asn
              555             560             565
  40
          AAA CTG TGC AAT GAT CCA AAG AAC ATG GTG TTC ATC GTT AGT GGA CGC     1779
          Lys Leu Cys Asn Asp Pro Lys Asn Met Val Phe Ile Val Ser Gly Arg
          570             575             580             585

  45      AGT AGA GAG AAA ATC TTG GCA GTT GGT TCG GCG CGT GTG AGA ACC CGC     1827
          Ser Arg Glu Lys Ile Leu Ala Val Gly Ser Ala Arg Val Arg Thr Arg
                          590             595             600

          CAT TGC ACT GAG CAC GGA TAC TTT ATA AGG TGG GCG GGT GAT CAA GAA     1875
  50      His Cys Thr Glu His Gly Tyr Phe Ile Arg Trp Ala Gly Asp Gln Glu
                          605             610             615
```

```
   TGG GAA ACG TGC GCA CGT GAG AAT AAT GTC GGG TGG ATG GAT GGA AAT      1923
   Trp Glu Thr Cys Ala Arg Glu Asn Asn Val Gly Trp Met Asp Gly Asn
       620             625             630

 5 CTG AGG CCG GTT ATG AAT CTT TAT ACA GAA ACT ACT GAC GGT TCG TAT      1971
   Leu Arg Pro Val Met Asn Leu Tyr Thr Glu Thr Thr Asp Gly Ser Tyr
       635             640             645

   ATT GAA AAG AAA GAA ACT GCA ATG GTT TGG CAC TAT GAA GAT GCT GAT      2019
10 Ile Glu Lys Lys Glu Thr Ala Met Val Trp His Tyr Glu Asp Ala Asp
   650             655             660             665

   AAA GAT CTT GGG TTG GAG CAG GCT AAG GAA CTG TTG GAC CAT CTT GAA      2067
   Lys Asp Leu Gly Leu Glu Gln Ala Lys Glu Leu Leu Asp His Leu Glu
15             670             675             680

   AAC GTG CTC GCT AAT GAG CCC GTT GGA GTG AAT CGA ACA GGT CAA TAC      2115
   Asn Val Leu Ala Asn Glu Pro Val Gly Val Asn Arg Thr Gly Gln Tyr
               685             690             695
20
   ATT GTA GAA GTT AAA CCA CAG TCC CCC ATT AAT TAC CTT CTT GTT ATG      2163
   Ile Val Glu Val Lys Pro Gln Ser Pro Ile Asn Tyr Leu Leu Val Met
       700             705             710

25 ACA TTC ATA GGC ACT GAT TGT AGA ATC TTT AAC TTA AAT TTC TTT AAA      2211
   Thr Phe Ile Gly Thr Asp Cys Arg Ile Phe Asn Leu Asn Phe Phe Lys
       715             720             725

   TAT GAA TGC AAT TAT AGG GGG TCA CTA AAA GGT ATA GTT GCA GAG AAG      2259
30 Tyr Glu Cys Asn Tyr Arg Gly Ser Leu Lys Gly Ile Val Ala Glu Lys
   730             735             740             745

   ATT TTT GCG TTC ATG GCT AAA AAG GGA AAA CAG GCT GAT TTC GTG TTG      2307
   Ile Phe Ala Phe Met Ala Lys Lys Gly Lys Gln Ala Asp Phe Val Leu
35             750             755             760

   ACG TTG AAT GAT AGA AGT GAT GAA GAC ATG TTT GTG GCC ATT GGG GAT      2355
   Thr Leu Asn Asp Arg Ser Asp Glu Asp Met Phe Val Ala Ile Gly Asp
               765             770             775
40
   GGA ATA AAA AAG GGT CGG ATA ACT AAC AAC AAT TCA GTG TTT ACA TGC      2403
   Gly Ile Lys Lys Gly Arg Ile Thr Asn Asn Asn Ser Val Phe Thr Cys
       780             785             790

45 GTA GTG GGA GAG AAA CCG AGT GCA GCT GAG TAC TTT TTA AAT GAT GTC      2451
   Val Val Gly Glu Lys Pro Ser Ala Ala Glu Tyr Phe Leu Asn Asp Val
       795             800             805

   TCG AGA AGC TCC GGG TGT CTC AGC AAC CAA GGA T GATCCGGAAG            2495
50 Ser Arg Ser Ser Gly Cys Leu Ser Asn Gln Gly
   810             815             820

   CTTCTCGTGA TCTTTATGAG TTAAAAGTTT TCGACTTTTT CTTCATCAAG ATTCATGGGA   2555
```

```
AAGTTGTTCA ATATGAACTT GTGTTCTTGG TTCTGGATTT TAGGGAGTCT ATGGATATAA      2615

CATTTC                                                                 2621
```

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 820 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ile Leu Leu His Leu Met Pro Leu Gln Met Leu Pro Asn Arg Leu
 1               5                  10                  15

Ile Val Val Ser Asn Gln Leu Pro Ile Ile Ala Arg Leu Arg Leu Thr
             20                  25                  30

Thr Met Glu Gly Pro Phe Gly Ile Ser Leu Gly Thr Arg Val Arg Phe
         35                  40                  45

Thr Cys Thr Ser Lys Met His Tyr Pro Gln Pro Leu Arg Phe Ser Ile
         50                  55                  60

Leu Gly Asp Pro Leu Arg Ala Asp Val Gly Pro Thr Glu Gln Asp Asp
     65                  70                  75                  80

Val Ser Lys Thr Leu Leu Asp Arg Phe Asn Cys Val Ala Val Phe Val
                 85                  90                  95

Pro Thr Ser Lys Trp Asp Gln Tyr Tyr His Cys Phe Cys Lys Gln Tyr
             100                 105                 110

Leu Trp Pro Ile Phe His Tyr Lys Val Pro Ala Ser Asp Val Lys Ser
         115                 120                 125

Val Pro Asn Ser Arg Asp Ser Trp Asn Ala Tyr Val His Val Asn Lys
     130                 135                 140

Glu Phe Ser Gln Lys Val Met Glu Ala Val Thr Asn Arg Ser Asn Tyr
 145                 150                 155                 160

Val Trp Ile His Asp Tyr His Leu Met Thr Leu Pro Thr Phe Leu Arg
             165                 170                 175

Arg Asp Phe Cys Arg Phe Lys Ile Gly Phe Phe Leu His Ser Pro Phe
         180                 185                 190

Pro Ser Ser Glu Val Tyr Lys Thr Leu Pro Met Arg Asn Glu Leu Leu
     195                 200                 205
```

34

```
    Lys Gly Leu Leu Asn Ala Asp Leu Ile Gly Phe His Thr Tyr Asp Tyr
        210                 215             220

 5  Ala Arg His Phe Leu Thr Cys Cys Ser Arg Met Phe Gly Leu Asp His
        225             230             235             240

    Gln Leu Lys Arg Gly Tyr Ile Phe Leu Glu Tyr Asn Gly Arg Ser Ile
                245             250             255
10
    Glu Ile Lys Ile Lys Ala Ser Gly Ile His Val Gly Arg Met Glu Ser
                260             265             270

    Tyr Leu Ser Gln Pro Asp Thr Arg Leu Gln Val Gln Glu Val Gln Lys
15          275             280             285

    Arg Ser Lys Glu Ile Val Leu Leu Gly Val Asp Asp Leu Asp Ile Phe
        290             295             300

20  Lys Gly Val Asn Phe Lys Val Leu Ala Leu Glu Lys Leu Leu Lys Ser
        305             310             315             320

    His Pro Ser Trp Gln Gly Arg Val Glu Lys Val Gln Ile Leu Asn Pro
                325             330             335
25
    Leu Arg Arg Cys Gln Asp Val Asp Glu Ile Asn Ala Glu Ile Arg Thr
                340             345             350

    Val Cys Glu Arg Ile Asn Asn Glu Leu Gly Ser Pro Gly Tyr Gln Pro
30          355             360             365

    Val Val Leu Ile Asp Gly Pro Val Ser Leu Ser Glu Lys Ala Ala Tyr
        370             375             380

35  Tyr Ala Ile Ala Asp Met Ala Ile Val Thr Pro Leu Arg Asp Gly Leu
        385             390             395             400

    Asn Leu Ile Pro Tyr Glu Tyr Val Val Ser Arg Gln Ser Val Asn Asp
                405             410             415
40
    Pro Asn Pro Asn Thr Pro Lys Lys Ser Met Leu Val Val Ser Glu Phe
                420             425             430

    Ile Gly Val Ser Leu Ser Leu Thr Gly Ala Ile Arg Val Asn Pro Trp
45          435             440             445

    Asp Glu Leu Glu Thr Ala Glu Ala Leu Tyr Asp Ala Leu Met Ala Pro
        450             455             460

50  Asp Asp His Lys Glu Thr Ala His Met Lys Gln Tyr Gln Tyr Ile Ile
        465             470             475             480

    Ser His Asp Val Ala Asn Trp Ala Ser Phe Phe Gln Asp Leu Glu Gln
                485             490             495
```

```
   Ala Cys Ile Asp His Ser Arg Lys Arg Cys Met Asn Leu Gly Phe Gly
           500             505             510

5  Leu Asp Thr Arg Val Val Phe Leu Met Arg Ser Leu Ala S r Trp Ile
           515             520             525

   Lys Met Ser Trp Lys Asn Ala Tyr Ser Met Ala Gln Asn Arg Ala Ile
           530             535             540
10
   Leu Leu Asp Tyr Asp Gly Thr Val Thr Pro Ser Ile Ser Lys Ser Pro
   545             550             555             560

   Thr Glu Ala Val Ile Ser Met Ile Asn Lys Leu Cys Asn Asp Pro Lys
15             565             570             575

   Asn Met Val Phe Ile Val Ser Gly Arg Ser Arg Glu Lys Ile Leu Ala
               580             585             590

20 Val Gly Ser Ala Arg Val Arg Thr Arg His Cys Thr Glu His Gly Tyr
           595             600             605

   Phe Ile Arg Trp Ala Gly Asp Gln Glu Trp Glu Thr Cys Ala Arg Glu
           610             615             620
25
   Asn Asn Val Gly Trp Met Asp Gly Asn Leu Arg Pro Val Met Asn Leu
   625             630             635             640

   Tyr Thr Glu Thr Thr Asp Gly Ser Tyr Ile Glu Lys Lys Glu Thr Ala
               645             650             655
30
   Met Val Trp His Tyr Glu Asp Ala Asp Lys Asp Leu Gly Leu Glu Gln
               660             665             670

35 Ala Lys Glu Leu Leu Asp His Leu Glu Asn Val Leu Ala Asn Glu Pro
           675             680             685

   Val Gly Val Asn Arg Thr Gly Gln Tyr Ile Val Glu Val Lys Pro Gln
   690             695             700
40
   Ser Pro Ile Asn Tyr Leu Leu Val Met Thr Phe Ile Gly Thr Asp Cys
   705             710             715             720

   Arg Ile Phe Asn Leu Asn Phe Phe Lys Tyr Glu Cys Asn Tyr Arg Gly
45             725             730             735

   Ser Leu Lys Gly Ile Val Ala Glu Lys Ile Phe Ala Phe Met Ala Lys
               740             745             750

50 Lys Gly Lys Gln Ala Asp Phe Val Leu Thr Leu Asn Asp Arg Ser Asp
           755             760             765

   Glu Asp Met Phe Val Ala Ile Gly Asp Gly Ile Lys Lys Gly Arg Ile
   770             775             780
```

```
     Thr Asn Asn Asn Ser Val Phe Thr Cys Val Val Gly Glu Lys Pro Ser
     785             790         795             800
```

5
```
     Ala Ala Glu Tyr Phe Leu Asn Asp Val Ser Arg Ser Ser Gly Cys Leu
                     805         810             815
```

```
     Ser Asn Gln Gly
                 820
```

10
```
     (2) INFORMATION FOR SEQ ID NO: 3:

         (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 25 base pairs
```
15
```
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: single
              (D)  TOPOLOGY: linear
```

```
         (ii) MOLECULE TYPE: DNA (genomic)
```
20
```
         (iii) HYPOTHETICAL: YES
```

```
         (iii) ANTI-SENSE: NO
```
25

```
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
```

```
     AAGCTTATGT TGCCATATAG AGTAG                                          25
```
30
```
     (2) INFORMATION FOR SEQ ID NO: 4:

         (i)  SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 24 base pairs
```
35
```
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: single
              (D)  TOPOLOGY: linear
```

```
         (ii) MOLECULE TYPE: DNA (genomic)
```
40
```
         (iii) HYPOTHETICAL: YES
```

```
         (iii) ANTI-SENSE: NO
```
45

```
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
```

```
     GTAGTTGCCA TGGTGCAAAT GTTC                                           24
```
50

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGCTCTGCAG TGAGGTACCA   20

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 20 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GACGTCACTC CATGGTTCGA   20

(2) INFORMATION FOR SEQ ID NO: 7:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 24 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTACCCTGCA GTGTGACCCT AGAC   24

(2) INFORMATION FOR SEQ ID NO: 8:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 21 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TCGATTCATA GAAGCTTAGA T   21

(2) INFORMATION FOR SEQ ID NO: 9:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2207 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA to mRNA

    (iii) HYPOTHETICAL: NO

    (iii) ANTI-SENSE: NO

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: Solanum tuberosum
        (B) STRAIN: Kardal

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 161..1906

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 842..850
        (D) OTHER INFORMATION: /function= "putative
            glycosylationsite"

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTTTTCTGAG TAATAACATA GGCATTGATT TTTTTTCAAT TAATAACACC TGCAAACATT   60

CCCATTGCCG GCATTCTCTG TTCTTACAAA AAAAAACATT TTTTTGTTCA CATAAATTAG   120

```
         TTATGGCATC AGTATTGAAC CCTTTAACTT GTTATACAAT ATG GGT AAA GCT ATA        175
                                                      Met Gly Lys Ala Ile
                                                       1                 5

  5  ATT TTT ATG ATT TTT ACT ATG TCT ATG AAT ATG ATT AAA GCT GAA ACT          223
     Ile Phe Met Ile Phe Thr Met Ser Met Asn Met Ile Lys Ala Glu Thr
             10                  15                  20

     TGC AAA TCC ATT GAT AAG GGT CCT GTA ATC CCA ACA ACC CCT TTA GTG          271
 10  Cys Lys Ser Ile Asp Lys Gly Pro Val Ile Pro Thr Thr Pro Leu Val
                 25                  30                  35

     ATT TTT CTT GAA AAA GTT CAA GAA GCT GCT CTT CAA ACT TAT GGC CAT          319
     Ile Phe Leu Glu Lys Val Gln Glu Ala Ala Leu Gln Thr Tyr Gly His
 15          40                  45                  50

     AAA GGG TTT GAT GCT AAA CTG TTT GTT GAT ATG TCA CTG AGA GAG AGT          367
     Lys Gly Phe Asp Ala Lys Leu Phe Val Asp Met Ser Leu Arg Glu Ser
             55                  60                  65
 20

     CTT TCA GAA ACA GTT GAA GCT TTT AAT AAG CTT CCA AGA GTT GTG AAT          415
     Leu Ser Glu Thr Val Glu Ala Phe Asn Lys Leu Pro Arg Val Val Asn
             70                  75                  80                  85

 25  GGT TCA ATA TCA AAA AGT GAT TTG GAT GGT TTT ATA GGT AGT TAC TTG          463
     Gly Ser Ile Ser Lys Ser Asp Leu Asp Gly Phe Ile Gly Ser Tyr Leu
                     90                  95                  100

     AGT AGT CCT GAT AAG GAT TTG GTT TAT GTT GAG CCT ATG GAT TTT GTG          511
 30  Ser Ser Pro Asp Lys Asp Leu Val Tyr Val Glu Pro Met Asp Phe Val
                    105                 110                 115

     GCT GAG CCT GAA GGC TTT TTG CCA AAG GTG AAG AAT TCT GAG GTG AGG          559
     Ala Glu Pro Glu Gly Phe Leu Pro Lys Val Lys Asn Ser Glu Val Arg
 35          120                 125                 130

     GCA TGG GCA TTG GAG GTG CAT TCA CTT TGG AAG AAT TTA AGT AGG AAA          607
     Ala Trp Ala Leu Glu Val His Ser Leu Trp Lys Asn Leu Ser Arg Lys
             135                 140                 145
 40

     GTG GCT GAT CAT GTA TTG GAA AAA CCA GAG TTG TAT ACT TTG CTT CCA          655
     Val Ala Asp His Val Leu Glu Lys Pro Glu Leu Tyr Thr Leu Leu Pro
     150                 155                 160                 165

 45  TTG AAA AAT CCA GTT ATT ATA CCG GGA TCG CGT TTT AAG GAG GTT TAT          703
     Leu Lys Asn Pro Val Ile Ile Pro Gly Ser Arg Phe Lys Glu Val Tyr
                     170                 175                 180

     TAT TGG GAT TCT TAT TGG GTA ATA AGG GGT TTG TTA GCA AGC AAA ATG          751
 50  Tyr Trp Asp Ser Tyr Trp Val Ile Arg Gly Leu Leu Ala Ser Lys Met
                     185                 190                 195
```

```
     TAT GAA ACT GCA AAA GGG ATT GTG ACT AAT CTG GTT TCT CTG ATA GAT        799
     Tyr Glu Thr Ala Lys Gly Ile Val Thr Asn Leu Val Ser Leu Ile Asp
             200                 205                 210

  5  CAA TTT GGT TAT GTT CTT AAC GGT GCA AGA GCA TAC TAC AGT AAC AGA        847
     Gln Phe Gly Tyr Val Leu Asn Gly Ala Arg Ala Tyr Tyr Ser Asn Arg
             215                 220                 225

     AGT CAG CCT CCT GTC CTG GCC ACG ATG ATT GTT GAC ATA TTC AAT CAG        895
 10  Ser Gln Pro Pro Val Leu Ala Thr Met Ile Val Asp Ile Phe Asn Gln
     230                 235                 240                 245

     ACA GGT GAT TTA AAT TTG GTT AGA AGA TCC CTT CCT GCT TTG CTC AAG        943
     Thr Gly Asp Leu Asn Leu Val Arg Arg Ser Leu Pro Ala Leu Leu Lys
 15                  250                 255                 260

     GAG AAT CAT TTT TGG AAT TCA GGA ATA CAT AAG GTG ACT ATT CAA GAT        991
     Glu Asn His Phe Trp Asn Ser Gly Ile His Lys Val Thr Ile Gln Asp
             265                 270                 275
 20
     GCT CAG GGA TCA AAC CAC AGC TTG AGT CGG TAC TAT GCT ATG TGG AAT       1039
     Ala Gln Gly Ser Asn His Ser Leu Ser Arg Tyr Tyr Ala Met Trp Asn
             280                 285                 290

 25  AAG CCC CGT CCA GAA TCG TCA ACT ATA GAC AGT GAA ACA GCT TCC GTA       1087
     Lys Pro Arg Pro Glu Ser Ser Thr Ile Asp Ser Glu Thr Ala Ser Val
             295                 300                 305

     CTC CCA AAT ATA TGT GAA AAA AGA GAA TTA TAC CGT GAA CTG GCA TCA       1135
 30  Leu Pro Asn Ile Cys Glu Lys Arg Glu Leu Tyr Arg Glu Leu Ala Ser
     310                 315                 320                 325

     GCT GCT GAA AGT GGA TGG GAT TTC AGT TCA AGA TGG ATG AGC AAC GGA       1183
     Ala Ala Glu Ser Gly Trp Asp Phe Ser Ser Arg Trp Met Ser Asn Gly
                     330                 335                 340
 35
     TCT GAT CTG ACA ACA ACT AGT ACA ACA TCA ATT CTA CCA GTT GAT TTG       1231
     Ser Asp Leu Thr Thr Thr Ser Thr Thr Ser Ile Leu Pro Val Asp Leu
                     345                 350                 355
 40
     AAT GCA TTC CTT CTG AAG ATG GAA CTT GAC ATT GCC TTT CTA GCA AAT       1279
     Asn Ala Phe Leu Leu Lys Met Glu Leu Asp Ile Ala Phe Leu Ala Asn
             360                 365                 370

 45  CTT GTT GGA GAA AGT AGC ACG GCT TCA CAT TTT ACA GAA GCT GCT CAA       1327
     Leu Val Gly Glu Ser Ser Thr Ala Ser His Phe Thr Glu Ala Ala Gln
             375                 380                 385

     AAT AGA CAG AAG GCT ATA AAC TGT ATC TTT TGG AAC GCA GAG ATG GGG       1375
 50  Asn Arg Gln Lys Ala Ile Asn Cys Ile Phe Trp Asn Ala Glu Met Gly
             390                 395                 400                 405
```

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      CAA TGG CTT GAT TAC TGG CTT ACC AAC AGC GAC ACA TCT GAG GAT ATT        1423
      Gln Trp Leu Asp Tyr Trp Leu Thr Asn Ser Asp Thr Ser Glu Asp Ile
                  410             415             420

 5    TAT AAA TGG GAA GAT TTG CAC CAG AAC AAG AAG TCA TTT GCC TCT AAT        1471
      Tyr Lys Trp Glu Asp Leu His Gln Asn Lys Lys Ser Phe Ala Ser Asn
                  425             430             435

      TTT GTT CCG CTG TGG ACT GAA ATT TCT TGT TCA GAT AAT AAT ATC ACA        1519
 10   Phe Val Pro Leu Trp Thr Glu Ile Ser Cys Ser Asp Asn Asn Ile Thr
                  440             445             450

      ACT CAG AAA GTA GTT CAA AGT CTC ATG AGC TCG GGC TTG CTT CAG CCT        1567
      Thr Gln Lys Val Val Gln Ser Leu Met Ser Ser Gly Leu Leu Gln Pro
 15       455             460             465

      GCA GGG ATT GCA ATG ACC TTG TCT AAT ACT GGA CAG CAA TGG GAT TTT        1615
      Ala Gly Ile Ala Met Thr Leu Ser Asn Thr Gly Gln Gln Trp Asp Phe
      470             475             480             485
 20
      CCG AAT GGT TGG CCC CCC CTT CAA CAC ATA ATC ATT GAA GGT CTC TTA        1663
      Pro Asn Gly Trp Pro Pro Leu Gln His Ile Ile Ile Glu Gly Leu Leu
                  490             495             500

 25   AGG TCT GGA CTA GAA GAG GCA AGA ACC TTA GCA AAA GAC ATT GCT ATT        1711
      Arg Ser Gly Leu Glu Glu Ala Arg Thr Leu Ala Lys Asp Ile Ala Ile
                  505             510             515

      CGC TGG TTA AGA ACT AAC TAT GTG ACT TAC AAG AAA ACC GGT GCT ATG        1759
 30   Arg Trp Leu Arg Thr Asn Tyr Val Thr Tyr Lys Lys Thr Gly Ala Met
                  520             525             530

      TAT GAA AAA TAT GAT GTC ACA AAA TGT GGA GCA TAT GGA GGT GGT GGT        1807
      Tyr Glu Lys Tyr Asp Val Thr Lys Cys Gly Ala Tyr Gly Gly Gly Gly
 35       535             540             545

      GAA TAT ATG TCC CAA ACG GGT TTC GGA TGG TCA AAT GGC GTT GTA CTG        1855
      Glu Tyr Met Ser Gln Thr Gly Phe Gly Trp Ser Asn Gly Val Val Leu
      550             555             560             565
 40
      GCA CTT CTA GAG GAA TTT GGA TGG CCT GAA GAT TTG AAG ATT GAT TGC        1903
      Ala Leu Leu Glu Glu Phe Gly Trp Pro Glu Asp Leu Lys Ile Asp Cys
                  570             575             580

 45   TAATGAGCAA GTAGAAAAGC CAAATGAAAC ATCATTGAGT TTTATTTTCT TCTTTTGTTA        1963

      AAATAAGCTG CAATGGTTTG CTGATAGTTT ATGTTTTGTA TTACTATTTC ATAAGGTTTT        2023

      TGTACCATAT CAAGTGATAT TACCATGAAC TATGTCGTTC GGACTCTTCA AATCGGATTT        2083
 50
      TGCAAAAATA ATGCAGTTTT GGAGAATCCG ATAACATAGA CCATGTATGG ATCTAAATTG        2143

      TAAACAGCTT ACTATATTAA GTAAAGAAA GATGATTCCT CTGCTTTAAA AAAAAAAAA        2203
```

AAAA   2207

(2) INFORMATION FOR SEQ ID NO: 10:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 581 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Gly Lys Ala Ile Ile Phe Met Ile Phe Thr Met Ser Met Asn Met
 1   5   10   15

Ile Lys Ala Glu Thr Cys Lys Ser Ile Asp Lys Gly Pro Val Ile Pro
                20   25   30

Thr Thr Pro Leu Val Ile Phe Leu Glu Lys Val Gln Glu Ala Ala Leu
                35   40   45

Gln Thr Tyr Gly His Lys Gly Phe Asp Ala Lys Leu Phe Val Asp Met
            50   55   60

Ser Leu Arg Glu Ser Leu Ser Glu Thr Val Glu Ala Phe Asn Lys Leu
 65   70   75   80

Pro Arg Val Val Asn Gly Ser Ile Ser Lys Ser Asp Leu Asp Gly Phe
                85   90   95

Ile Gly Ser Tyr Leu Ser Ser Pro Asp Lys Asp Leu Val Tyr Val Glu
                100   105   110

Pro Met Asp Phe Val Ala Glu Pro Glu Gly Phe Leu Pro Lys Val Lys
            115   120   125

Asn Ser Glu Val Arg Ala Trp Ala Leu Glu Val His Ser Leu Trp Lys
            130   135   140

Asn Leu Ser Arg Lys Val Ala Asp His Val Leu Glu Lys Pro Glu Leu
145   150   155   160

Tyr Thr Leu Leu Pro Leu Lys Asn Pro Val Ile Ile Pro Gly Ser Arg
                165   170   175

Phe Lys Glu Val Tyr Tyr Trp Asp Ser Tyr Trp Val Ile Arg Gly Leu
                180   185   190

Leu Ala Ser Lys Met Tyr Glu Thr Ala Lys Gly Ile Val Thr Asn Leu
            195   200   205

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      Val Ser Leu Ile Asp Gln Phe Gly Tyr Val Leu Asn Gly Ala Arg Ala
          210             215         220

      Tyr Tyr Ser Asn Arg Ser Gln Pro Pro Val Leu Ala Thr Met Ile Val
  5   225             230             235                 240

      Asp Ile Phe Asn Gln Thr Gly Asp Leu Asn Leu Val Arg Arg Ser Leu
                  245             250                 255

 10   Pro Ala Leu Leu Lys Glu Asn His Phe Trp Asn Ser Gly Ile His Lys
                  260             265                 270

      Val Thr Ile Gln Asp Ala Gln Gly Ser Asn His Ser Leu Ser Arg Tyr
                  275             280                 285

 15
      Tyr Ala Met Trp Asn Lys Pro Arg Pro Glu Ser Ser Thr Ile Asp Ser
          290             295             300

      Glu Thr Ala Ser Val Leu Pro Asn Ile Cys Glu Lys Arg Glu Leu Tyr
 20   305             310             315                 320

      Arg Glu Leu Ala Ser Ala Ala Glu Ser Gly Trp Asp Phe Ser Ser Arg
                  325             330                 335

 25   Trp Met Ser Asn Gly Ser Asp Leu Thr Thr Thr Ser Thr Thr Ser Ile
                  340             345                 350

      Leu Pro Val Asp Leu Asn Ala Phe Leu Leu Lys Met Glu Leu Asp Ile
                  355             360                 365

 30
      Ala Phe Leu Ala Asn Leu Val Gly Glu Ser Ser Thr Ala Ser His Phe
          370             375             380

      Thr Glu Ala Ala Gln Asn Arg Gln Lys Ala Ile Asn Cys Ile Phe Trp
 35   385             390             395                 400

      Asn Ala Glu Met Gly Gln Trp Leu Asp Tyr Trp Leu Thr Asn Ser Asp
                  405             410                 415

 40   Thr Ser Glu Asp Ile Tyr Lys Trp Glu Asp Leu His Gln Asn Lys Lys
                  420             425                 430

      Ser Phe Ala Ser Asn Phe Val Pro Leu Trp Thr Glu Ile Ser Cys Ser
          435             440             445

 45
      Asp Asn Asn Ile Thr Thr Gln Lys Val Val Gln Ser Leu Met Ser Ser
          450             455             460

      Gly Leu Leu Gln Pro Ala Gly Ile Ala Met Thr Leu Ser Asn Thr Gly
 50   465             470             475                 480

      Gln Gln Trp Asp Phe Pro Asn Gly Trp Pro Pro Leu Gln His Ile Ile
                  485             490                 495
```

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Il  Glu Gly Leu Leu Arg Ser Gly Leu Glu Glu Ala Arg Thr Leu Ala
            500                 505             510

Lys Asp Ile Ala Ile Arg Trp Leu Arg Thr Asn Tyr Val Thr Tyr Lys
        515             520             525

Lys Thr Gly Ala Met Tyr Glu Lys Tyr Asp Val Thr Lys Cys Gly Ala
    530                 535             540

Tyr Gly Gly Gly Gly Glu Tyr Met Ser Gln Thr Gly Phe Gly Trp Ser
545                 550             555                 560

Asn Gly Val Val Leu Ala Leu Leu Glu Glu Phe Gly Trp Pro Glu Asp
                565             570             575

Leu Lys Ile Asp Cys
            580
```

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: DNA (genomic)

    (iii) HYPOTHETICAL: YES

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 6
        (D) OTHER INFORMATION: /mod_base= i

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 15
        (D) OTHER INFORMATION: /mod_base= i

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGYGGNMGMT TYRWNGARKT MTAYKRYTGG GAC   33

(2) INFORMATION FOR SEQ ID NO: 12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 26 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: YES

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 3
               (D) OTHER INFORMATION: /mod_base= i

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 6
               (D) OTHER INFORMATION: /mod_base= i

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 9
               (D) OTHER INFORMATION: /mod_base= i

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 12
               (D) OTHER INFORMATION: /mod_base= i

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 15
               (D) OTHER INFORMATION: /mod_base= i

          (ix) FEATURE:
               (A) NAME/KEY: modified_base
               (B) LOCATION: 21
               (D) OTHER INFORMATION: /mod_base= i

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTNCCNGGNG GNCGNTTYRW NGARKT   26

     (2) INFORMATION FOR SEQ ID NO: 13:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 26 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

          (iii) HYPOTHETICAL: YES

```
        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 3
              (D)  OTHER INFORMATION: /mod_base= i

        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 9
              (D)  OTHER INFORMATION: /mod_base= i

        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 12
              (D)  OTHER INFORMATION: /mod_base= i

        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 15
              (D)  OTHER INFORMATION: /mod_base= i

        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 18
              (D)  OTHER INFORMATION: /mod_base= i


        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 13:

   GGNGGYTGNS WNCGNYRNAG RTARTA                             26

   (2)  INFORMATION FOR SEQ ID NO: 14:

        (i)   SEQUENCE CHARACTERISTICS:
              (A)  LENGTH: 24 base pairs
              (B)  TYPE: nucleic acid
              (C)  STRANDEDNESS: single
              (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: DNA (genomic)

        (iii) HYPOTHETICAL: YES


        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 1
              (D)  OTHER INFORMATION: /mod_base= i

        (ix)  FEATURE:
              (A)  NAME/KEY: modified_base
              (B)  LOCATION: 7
              (D)  OTHER INFORMATION: /mod_base= i
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(ix) FEATURE:
     (A) NAME/KEY: modified_base
     (B) LOCATION: 19
     (D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
     (A) NAME/KEY: modified_base
     (B) LOCATION: 22
     (D) OTHER INFORMATION: /mod_base= i


(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

NSCRTTNRYC CATCCRAANC CNTC

(2) INFORMATION FOR SEQ ID NO: 15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (iii) HYPOTHETICAL: NO



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGAAACGGGC CCATCAATTA

(2) INFORMATION FOR SEQ ID NO: 16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (iii) HYPOTHETICAL: NO



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TCGATGAGAT CAATGCCGAG
```

24

20

20

(2) INFORMATION FOR SEQ ID NO: 17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
5   (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA
10

    (iii) HYPOTHETICAL: NO

15   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CCATCCTAAT ACGACTCACT ATAGGGC   27

(2) INFORMATION FOR SEQ ID NO: 18:
20
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO
30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

35 CACAACAGGC TGGTATCCCG   20

(2) INFORMATION FOR SEQ ID NO: 19:

    (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

45   (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

50
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAATAACGAA CTGGGAAGCC   20

(2) INFORMATION FOR SEQ ID NO: 20:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 23 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

 (iii) HYPOTHETICAL: NO

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACTCACTATA GGGCTCGAGC GGC   23

(2) INFORMATION FOR SEQ ID NO: 21:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 26 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: single
       (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: cDNA

 (iii) HYPOTHETICAL: NO

  (ix) FEATURE:
       (A) NAME/KEY: modified_base
       (B) LOCATION: 4
       (D) OTHER INFORMATION: /mod_base= i

  (ix) FEATURE:
       (A) NAME/KEY: modified_base
       (B) LOCATION: 6
       (D) OTHER INFORMATION: /mod_base= i

  (ix) FEATURE:
       (A) NAME/KEY: modified_base
       (B) LOCATION: 9
       (D) OTHER INFORMATION: /mod_base= i

  (ix) FEATURE:
       (A) NAME/KEY: modified_base
       (B) LOCATION: 15
       (D) OTHER INFORMATION: /mod_base= i

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GAYNTNATNT GGRTNCAYGA YTAYCA   26

(2) INFORMATION FOR SEQ ID NO: 22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 3
        (D) OTHER INFORMATION: /mod_base= i

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 6
        (D) OTHER INFORMATION: /mod_base= i

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 12
        (D) OTHER INFORMATION: /mod_base= i

    (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 18
        (D) OTHER INFORMATION: /mod_base= i

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCNACNGTRC ANGCRAANAC   20

(2) INFORMATION FOR SEQ ID NO: 23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 28 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO

```
    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 2
          (D)  OTHER INFORMATION: /mod_base= i

    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 5
          (D)  OTHER INFORMATION: /mod_base= i

    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 8
          (D)  OTHER INFORMATION: /mod_base= i

    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 14
          (D)  OTHER INFORMATION: /mod_base= i

    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 20
          (D)  OTHER INFORMATION: /mod_base= i

    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 23
          (D)  OTHER INFORMATION: /mod_base= i


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TNGGNTKNTT YYTNCAYAYN CCNTTYCC                                        28

    (2)  INFORMATION FOR SEQ ID NO: 24:

    (i)   SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 20 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: single
          (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: cDNA

    (iii) HYPOTHETICAL: NO


    (ix)  FEATURE:
          (A)  NAME/KEY: modified_base
          (B)  LOCATION: 6
          (D)  OTHER INFORMATION: /mod_base= i
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(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 9
    (D) OTHER INFORMATION: /mod_base= i

5

(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 18
    (D) OTHER INFORMATION: /mod_base= i

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TGRTCNARNA RYTCYTTNGC

15

20

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 20 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

25

(iii) HYPOTHETICAL: NO

(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 9
    (D) OTHER INFORMATION: /mod_base= i

30

(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 12
    (D) OTHER INFORMATION: /mod_base= i

35

(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 15
    (D) OTHER INFORMATION: /mod_base= i

40

(ix) FEATURE:
    (A) NAME/KEY: modified_base
    (B) LOCATION: 18
    (D) OTHER INFORMATION: /mod_base= i

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCRTGYTCNG CNSWNARNCC

20

(2) INFORMATION FOR SEQ ID NO: 26:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (iii) HYPOTHETICAL: NO

   (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 6
        (D) OTHER INFORMATION: /mod_base= i

   (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 17
        (D) OTHER INFORMATION: /mod_base= i

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TCRTCNGTRA ARTCRTCNCC   20

(2) INFORMATION FOR SEQ ID NO: 27:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (iii) HYPOTHETICAL: NO

   (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 3
        (D) OTHER INFORMATION: /mod_base= i

   (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 6
        (D) OTHER INFORMATION: /mod_base= i

   (ix) FEATURE:
        (A) NAME/KEY: modified_base
        (B) LOCATION: 15

(D) OTHER INFORMATION: /mod_base= i

     (ix) FEATURE:
           (A) NAME/KEY: modified_base
5   (B) LOCATION: 21
           (D) OTHER INFORMATION: /mod_base= i

10   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

     GYNACNARRT TCATNCCRTC NC   22

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:
    (A) NAME/KEY: modified_base
5   (B) LOCATION: 21
    (D) OTHER INFORMATION: /mod_base= i

10   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GYNACNARRT TCATNCCRTC NC

22